nucleic acid probe of greater than about 50,000 bases in *in situ* hybridization, wherein the chromosomal material is present in a morphologically identifiable [chromosome or] cell nucleus; allowing said probe to bind to said targeted chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

48. (Twice Amended) A method of staining targeted interphase chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein said targeted chromosomal material is a genetic rearrangement associated with chromosome 3 and/or chromosome 17 in humans, said method comprising contacting said chromosomal material with a unique sequence high complexity nucleic acid probe of greater than about 40 kb, wherein the chromosomal material is present in a morphologically identifiable [chromosome or] cell nucleus; allowing said probe to bind to said targeted chromosomal material; and detecting said bound probe, wherein bound probe is indicative of the presence of target chromosomal material.

50. (Twice Amended) A method of staining targeted interphase chromosomal material based upon a nucleic acid segment employing a unique sequence high complexity nucleic acid probe of greater than about 50,000 bases, wherein said targeted interphase chromosomal material is a genetic rearrangement associated